

## RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number:

09/532,263A

Source:

IFW/6

Date Processed by STIC:

3-30-05

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 03/30/2005

PATENT APPLICATION: US/09/532,263A

TIME: 10:35:32

Input Set : A:\10296A.sub.seq.txt

Output Set: N:\CRF4\03302005\I532263A.raw

## SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Hilton, Douglas J.

7 (ii) TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR

9 (iii) NUMBER OF SEQUENCES: 25

11 (iv) CORRESPONDENCE ADDRESS:

13 (A) ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER

14 (B) STREET: 400 Garden City Plaza

15 (C) CITY: Garden City

16 (D) STATE: New York

17 (E) COUNTRY: United States of America

18 (F) ZIP: 11530

20 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

27 (vi) CURRENT APPLICATION DATA:

C--> 29 (A) APPLICATION NUMBER: US/09/532,263A

C--> 30 (B) FILING DATE: 22-Mar-2000

31 (C) CLASSIFICATION:

33 (viii) ATTORNEY/AGENT INFORMATION:

35 (A) NAME: Presser, Leopold

36 (B) REGISTRATION NUMBER: 19,827

37 (C) REFERENCE/DOCKET NUMBER: 10296

39 (ix) TELECOMMUNICATION INFORMATION:

41 (A) TELEPHONE: (516) 742-4343

42 (B) TELEFAX: (516) 742-4366

43 (C) TELEX: 203 901 SANS UR

45 (2) INFORMATION FOR SEQ ID NO: 1:

47 (i) SEQUENCE CHARACTERISTICS:

49 (A) LENGTH: 5 amino acids

50 (B) TYPE: amino acid

51 (C) STRANDEDNESS: single

52 (D) TOPOLOGY: linear

54 (ii) MOLECULE TYPE: DNA (genomic)

56 (ix) FEATURE:

57 (A) NAME/KEY: misc\_feature

58 (B) LOCATION: 3..3

59 (D) OTHER INFORMATION: /note= "Xaa at Position 3 is any amino acid"

61 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

W--> 63 Trp Ser Xaa Trp Ser

64 1 5

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66 (2) INFORMATION FOR SEQ ID NO: 2:

68 (i) SEQUENCE CHARACTERISTICS:

70 (A) LENGTH: 1705 base pairs

71 (B) TYPE: nucleic acid

72 (C) STRANDEDNESS: single

73 (D) TOPOLOGY: linear

75 (ii) MOLECULE TYPE: DNA (genomic)

77 (ix) FEATURE:

79 (A) NAME/KEY: CDS

80 (B) LOCATION: 45..1340

82 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

84 GAGAGGGTGA GGGCGGAGGC CGCTGGCGGC GGCTGCCGCA GAAG ATG AGC AGC AGC      56
85                                     Met Ser Ser Ser
86                                     1
88 TGC TCA GGG CTG ACC AGG GTC CTG GTG GCC GTG GCT ACA GCC CTG GTG      104
89 Cys Ser Gly Leu Thr Arg Val Leu Val Ala Val Ala Thr Ala Leu Val
90   5          10          15          20
92 TCT TCC TCC TCC CCC TGC CCC CAA GCT TGG GGT CCT CCA GGG GTC CAG      152
93 Ser Ser Ser Ser Pro Cys Pro Gln Ala Trp Gly Pro Pro Gly Val Gln
94          25          30          35
96 TAT GGA CAA CCT GGC AGG CCC GTG ATG CTG TGC TGC CCC GGA GTG AGT      200
97 Tyr Gly Gln Pro Gly Arg Pro Val Met Leu Cys Cys Pro Gly Val Ser
98          40          45          50
100 GCT GGG ACT CCA GTG TCC TGG TTT CGG GAT GGA GAT TCA AGG CTG CTC      248
101 Ala Gly Thr Pro Val Ser Trp Phe Arg Asp Gly Asp Ser Arg Leu Leu
102          55          60          65
104 CAG GGA CCT GAC TCT GGG TTA GGA CAC AGA CTG GTC TTG GCC CAG GTG      296
105 Gln Gly Pro Asp Ser Gly Leu Gly His Arg Leu Val Leu Ala Gln Val
106          70          75          80
108 GAC AGC CCT GAT GAA GGC ACT TAT GTC TGC CAG ACC CTG GAT GGT GTA      344
109 Asp Ser Pro Asp Glu Gly Thr Tyr Val Cys Gln Thr Leu Asp Gly Val
110  85          90          95          100
112 TCA GGG GGC ATG GTG ACC CTG AAG CTG GGC TTT CCC CCA GCA CGT CCT      392
113 Ser Gly Gly Met Val Thr Leu Lys Leu Gly Phe Pro Pro Ala Arg Pro
114          105          110          115
116 GAA GTC TCC TGC CAA GCG GTA GAC TAT GAA AAC TTC TCC TGT ACT TGG      440
117 Glu Val Ser Cys Gln Ala Val Asp Tyr Glu Asn Phe Ser Cys Thr Trp
118          120          125          130
120 AGT CCA GGC CAG GTC AGC GGT TTG CCC ACC CGC TAC CTT ACT TCC TAC      488
121 Ser Pro Gly Gln Val Ser Gly Leu Pro Thr Arg Tyr Leu Thr Ser Tyr
122          135          140          145
124 AGG AAG AAG ACG CTG CCA GGA GCT GAG AGT CAG AGG GAA AGT CCA TCC      536
125 Arg Lys Lys Thr Leu Pro Gly Ala Glu Ser Gln Arg Glu Ser Pro Ser
126          150          155          160
128 ACC GGG CCT TGG CCG TGT CCA CAG GAC CCT CTG GAG GCC TCC CGA TGT      584
129 Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro Leu Glu Ala Ser Arg Cys
130 165          170          175          180
132 GTG GTC CAT GGG GCA GAG TTC TGG AGT GAG TAC CGG ATC AAT GTG ACC      632
133 Val Val His Gly Ala Glu Phe Trp Ser Glu Tyr Arg Ile Asn Val Thr

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134	185	190	195	
136	GAG GTG AAC CCA CTG GGT GCC AGC ACG TGC CTA CTG GAT GTG AGA TTA	680		
137	Glu Val Asn Pro Leu Gly Ala Ser Thr Cys Leu Leu Asp Val Arg Leu			
138	200 205 210			
140	CAG AGC ATC TTG CGT CCT GAT CCA CCC CAA GGA CTG CGG GTG GAA TCC	728		
141	Gln Ser Ile Leu Arg Pro Asp Pro Pro Gln Gly Leu Arg Val Glu Ser			
142	215 220 225			
144	GTA CCT GGT TAC CCG AGA CGC CTG CAT GCC AGC TGG ACA TAC CCT GCC	776		
145	Val Pro Gly Tyr Pro Arg Arg Leu His Ala Ser Trp Thr Tyr Pro Ala			
146	230 235 240			
148	TCC TGG CGT CGC CAA CCC CAC TTT CTG CTC AAG TTC CGG TTG CAA TAC	824		
149	Ser Trp Arg Arg Gln Pro His Phe Leu Leu Lys Phe Arg Leu Gln Tyr			
150	245 250 255 260			
152	CGA CCA GCA CAG CAT CCA GCC TGG TCC ACG GTG GAG CCC ATT GGC TTG	872		
153	Arg Pro Ala Gln His Pro Ala Trp Ser Thr Val Glu Pro Ile Gly Leu			
154	265 270 275			
156	GAG GAA GTG ATA ACA GAT GCT GTG GCT GGG CTG CCA CAC GCG GTA CGA	920		
157	Glu Glu Val Ile Thr Asp Ala Val Ala Gly Leu Pro His Ala Val Arg			
158	280 285 290			
160	GTC AGT GCC AGG GAC TTT CTG GAT GCT GGC ACC TGG AGC GCC TGG AGC	968		
161	Val Ser Ala Arg Asp Phe Leu Asp Ala Gly Thr Trp Ser Ala Trp Ser			
162	295 300 305			
164	CCA GAG GCC TGG GGT ACT CCT AGC ACT GGT CCC CTG CAG GAT GAG ATA	1016		
165	Pro Glu Ala Trp Gly Thr Pro Ser Thr Gly Pro Leu Gln Asp Glu Ile			
166	310 315 320			
168	CCT GAT TGG AGC CAG GGA CAT GGA CAG CAG CTA GAG GCA GTA GTA GCT	1064		
169	Pro Asp Trp Ser Gln Gly His Gly Gln Gln Leu Glu Ala Val Val Ala			
170	325 330 335 340			
171	CAG GAG GAC AGC CCG GCT CCT GCA AGG CCT TCC TTG CAG CCG GAC CCA	1112		
172	Gln Glu Asp Ser Pro Ala Pro Ala Arg Pro Ser Leu Gln Pro Asp Pro			
173	345 350 355			
175	AGG CCA CTT GAT CAC AGG GAC CCC TTG GAG CAA GTA GCT GTG TTA GCG	1160		
176	Arg Pro Leu Asp His Arg Asp Pro Leu Glu Gln Val Ala Val Leu Ala			
177	360 365 370			
179	TCT CTG GGA ATC TTC TCT TGC CTT GGC CTG GCT GTT GGA GCT CTG GCA	1208		
180	Ser Leu Gly Ile Phe Ser Cys Leu Gly Leu Ala Val Gly Ala Leu Ala			
181	375 380 385			
183	CTG GGG CTC TGG CTG AGG CTG AGA CGG AGT GGG AAG GAT GGA CCG CAA	1256		
184	Leu Gly Leu Trp Leu Arg Leu Arg Arg Ser Gly Lys Asp Gly Pro Gln			
185	390 395 400			
187	AAA CCT GGG CTC TTG GCA CCC ATG ATC CCG GTG GAA AAG CTT CCA GGA	1304		
188	Lys Pro Gly Leu Leu Ala Pro Met Ile Pro Val Glu Lys Leu Pro Gly			
189	405 410 415 420			
191	ATT CCA AAC CTG CAG AGG ACC CCA GAG AAC TTC AGC TGATTTTCATC	1350		
192	Ile Pro Asn Leu Gln Arg Thr Pro Glu Asn Phe Ser			
193	425 430			
195	TGTAACCCGG TCAGACTGGG GGCAGAAAGA GGCGGGGCAG TGGATCCCTG TGGATGGAGG	1410		
197	TCTCAGCTGA AAGTCTGAGC TCTTTTCTTT GACACCTATA CTCCAAACTT GCTGCCGGCT	1470		
199	GAAGGCTGTC TGGACTTCCG ATGTCCTGAG GTGGAAGTCC ACCTGAGGAA TGTGTACAGA	1530		

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201 AGTCTGTGTT CCTGTGATCG TGTGTGTATG TGAGACAGGG AGCAAAAGTT CTCTGCATGT      1590
203 GTGTACAGAT GATTGGAGAG TGTGTGCGGT CTTGGGCTTG GCCCTTCTGG GAAGTGTGAA      1650
205 GAGTTGAAAT AAAAGAGACG GAAGTTTTTG GAAAAAAAAA AAAAAAAAAA AAAAAA      1705
207 (2) INFORMATION FOR SEQ ID NO: 3:
209     (i) SEQUENCE CHARACTERISTICS:
211         (A) LENGTH: 432 amino acids
212         (B) TYPE: amino acid
213         (D) TOPOLOGY: linear
215     (ii) MOLECULE TYPE: protein
217     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
219 Met Ser Ser Ser Cys Ser Gly Leu Thr Arg Val Leu Val Ala Val Ala
220 1      5      10      15
222 Thr Ala Leu Val Ser Ser Ser Ser Pro Cys Pro Gln Ala Trp Gly Pro
223      20      25      30
225 Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Pro Val Met Leu Cys Cys
226      35      40      45
228 Pro Gly Val Ser Ala Gly Thr Pro Val Ser Trp Phe Arg Asp Gly Asp
229      50      55      60
231 Ser Arg Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly His Arg Leu Val
232      65      70      75      80
234 Leu Ala Gln Val Asp Ser Pro Asp Glu Gly Thr Tyr Val Cys Gln Thr
235      85      90      95
237 Leu Asp Gly Val Ser Gly Gly Met Val Thr Leu Lys Leu Gly Phe Pro
238      100     105     110
240 Pro Ala Arg Pro Glu Val Ser Cys Gln Ala Val Asp Tyr Glu Asn Phe
241      115     120     125
243 Ser Cys Thr Trp Ser Pro Gly Gln Val Ser Gly Leu Pro Thr Arg Tyr
244      130     135     140
246 Leu Thr Ser Tyr Arg Lys Lys Thr Leu Pro Gly Ala Glu Ser Gln Arg
247 145     150     155     160
249 Glu Ser Pro Ser Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro Leu Glu
250      165     170     175
252 Ala Ser Arg Cys Val Val His Gly Ala Glu Phe Trp Ser Glu Tyr Arg
253      180     185     190
255 Ile Asn Val Thr Glu Val Asn Pro Leu Gly Ala Ser Thr Cys Leu Leu
256      195     200     205
258 Asp Val Arg Leu Gln Ser Ile Leu Arg Pro Asp Pro Pro Gln Gly Leu
259      210     215     220
261 Arg Val Glu Ser Val Pro Gly Tyr Pro Arg Arg Leu His Ala Ser Trp
262 225     230     235     240
264 Thr Tyr Pro Ala Ser Trp Arg Arg Gln Pro His Phe Leu Leu Lys Phe
265      245     250     255
267 Arg Leu Gln Tyr Arg Pro Ala Gln His Pro Ala Trp Ser Thr Val Glu
268      260     265     270
270 Pro Ile Gly Leu Glu Glu Val Ile Thr Asp Ala Val Ala Gly Leu Pro
271      275     280     285
273 His Ala Val Arg Val Ser Ala Arg Asp Phe Leu Asp Ala Gly Thr Trp
274      290     295     300
276 Ser Ala Trp Ser Pro Glu Ala Trp Gly Thr Pro Ser Thr Gly Pro Leu

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277 305          310          315          320
279 Gln Asp Glu Ile Pro Asp Trp Ser Gln Gly His Gly Gln Gln Leu Glu
280          325          330          335
282 Ala Val Val Ala Gln Glu Asp Ser Pro Ala Pro Ala Arg Pro Ser Leu
283          340          345          350
285 Gln Pro Asp Pro Arg Pro Leu Asp His Arg Asp Pro Leu Glu Gln Val
286          355          360          365
288 Ala Val Leu Ala Ser Leu Gly Ile Phe Ser Cys Leu Gly Leu Ala Val
289          370          375          380
291 Gly Ala Leu Ala Leu Gly Leu Trp Leu Arg Leu Arg Arg Ser Gly Lys
292 385          390          395          400
294 Asp Gly Pro Gln Lys Pro Gly Leu Leu Ala Pro Met Ile Pro Val Glu
295          405          410          415
297 Lys Leu Pro Gly Ile Pro Asn Leu Gln Arg Thr Pro Glu Asn Phe Ser
298          420          425          430
301 (2) INFORMATION FOR SEQ ID NO: 4:
303     (i) SEQUENCE CHARACTERISTICS:
305         (A) LENGTH: 1800 base pairs
306         (B) TYPE: nucleic acid
307         (C) STRANDEDNESS: single
308         (D) TOPOLOGY: linear
310     (ii) MOLECULE TYPE: cDNA
312     (iii) HYPOTHETICAL: NO
314     (iv) ANTI-SENSE: NO
317     (ix) FEATURE:
319         (A) NAME/KEY: CDS
320         (B) LOCATION: 128..1396
322     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
324 TCTAACAGCC TTACCCCACT TGGTGCATCA ATTTTCTCC TAGGAAGCCT CAGTTTGGGA      60
326 GAGGAAGAGC CAGGCTTTAG CTCCCATCTC AGGGGTCGGG GATTTTGTAC TCTACCTCTC      120
328 CCCACAG ATG AGC AGC AGC TGC TCA GGG CTG AGC AGG GTC CTG GTG GCC      169
329 Met Ser Ser Ser Cys Ser Gly Leu Ser Arg Val Leu Val Ala
330 1 5 10
332 GTG GCT ACA GCC CTG GTG TCT GCC TCC TCC CCC TGC CCC CAG GCC TGG      217
333 Val Ala Thr Ala Leu Val Ser Ala Ser Ser Pro Cys Pro Gln Ala Trp
334 15 20 25 30
336 GGC CCC CCA GGG GTC CAG TAT GGG CAG CCA GGC AGG TCC GTG AAG CTG      265
337 Gly Pro Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Ser Val Lys Leu
338 35 40 45
340 TGT TGT CCT GGA GTG ACT GCC GGG GAC CCA GTG TCC TGG TTT CGG GAT      313
341 Cys Cys Pro Gly Val Thr Ala Gly Asp Pro Val Ser Trp Phe Arg Asp
342 50 55 60
344 GGG GAG CCA AAG CTG CTC CAG GGA CCT GAC TCT GGG CTA GGG CAT GAA      361
345 Gly Glu Pro Lys Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly His Glu
346 65 70 75
348 CTG GTC CTG GCC CAG GCA GAC AGC ACT GAT GAG GGC ACC TAC ATC TGC      409
349 Leu Val Leu Ala Gln Ala Asp Ser Thr Asp Glu Gly Thr Tyr Ile Cys
350 80 85 90
352 CAG ACC CTG GAT GGT GCA CTT GGG GGC ACA GTG ACC CTG CAG CTG GGC      457

```

RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 03/30/2005  
PATENT APPLICATION: US/09/532,263A      TIME: 10:35:33

Input Set : A:\10296A.sub.seq.txt  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos.3 ✓  
Seq#:8; N Pos. 7  
Seq#:9; N Pos. 7  
Seq#:23; N Pos. 7

## VERIFICATION SUMMARY

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Input Set : A:\10296A.sub.seq.txt

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L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:63 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0